GenCore version 5.1.7

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 08:29:11 ; Search time 3415 Seconds
(without alignments)
1959.166 Million cell updates/sec

Title: US-10-759-548B-5
Perfect score: 706
Sequence: 1 MALSLSLARPAPLAVSAGAG.....SDYDNVTGALPYLKVNRKAN 143

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10759548/runat_02032006_160942_17044/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absa07
-USER=US10759548_@CGN_1_1_6731_@runat_02032006_160942_17044 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	706	100.0	443	3	BI358791	BI358791 949040H08
c	2	706	100.0	555	3	BI478792	BI478792 949070F06
c	3	706	100.0	593	3	BI993293	BI993293 1020075G1
	4	706	100.0	803	1	AI001298	AI001298 MEST6-D3.
	5	706	100.0	868	4	AY108827	AY108827 Zea mays
	6	687	97.3	554	2	BG410559	BG410559 947050C09
	7	686.5	97.2	643	7	CN141441	CN141441 OX1_51_D0
	8	679	96.2	626	5	BQ635741	BQ635741 1091071H1
	9	678.5	96.1	731	6	CA236566	CA236566 SCSBFL501
	10	675.5	95.7	525	6	CA128302	CA128302 SCJFLR203
	11	673	95.3	430	2	BI233829	BI233829 949032H11
	12	658	93.2	412	2	BG317125	BG317125 947025F08
	13	656.5	93.0	573	8	DN144120	DN144120 4816_H11
	14	654	92.6	538	2	BG354513	BG354513 947038C07
	15	654	92.6	542	5	BU092662	BU092662 946155D06
c	16	650	92.1	755	2	BG320303	BG320303 Zm03_12e0
c	17	641	90.8	499	3	BI359221	BI359221 949040H08
	18	623.5	88.3	540	6	CA301023	CA301023 SCRLLV105
c	19	623	88.2	489	2	BG549199	BG549199 947073E08
	20	612	86.7	482	2	BG458495	BG458495 947044G05
	21	585	82.9	363	2	BI096564	BI096564 949012C10
c	22	576	81.6	871	1	AI374506	AI374506 MEST6-D3.
	23	558	79.0	396	2	BG458566	BG458566 947045G01
c	24	547	77.5	606	2	BG462527	BG462527 947057H09
c	25	530.5	75.1	819	10	CZ296823	CZ296823 ZMMBF0066
	26	529	74.9	336	3	BI478541	BI478541 949070P06
	27	523	74.1	335	2	BG462521	BG462521 947057H05
c	28	521	73.8	387	2	BG550202	BG550202 947038C07
c	29	507.5	71.9	685	10	CW239849	CW239849 104_698_1
c	30	502	71.1	469	3	BM380889	BM380889 MEST526-F
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	32	497.5	70.5	508	7	CF953034	CF953034 693rsiceb
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	34	497	70.4	349	2	BG549200	BG549200 947073E08
	35	495.5	70.2	536	7	CF955858	CF955858 4852rsice
	36	482	68.3	357	2	BG316582	BG316582 947021A01
c	37	468	66.3	563	2	BG462520	BG462520 947057H05
	38	466.5	66.1	551	6	CA500123	CA500123 WHE4015_F
	39	466.5	66.1	579	2	BE425970	BE425970 WHE0326_C
	40	466.5	66.1	596	3	BM134808	BM134808 WHE0453_H
	41	466.5	66.1	627	6	CA499879	CA499879 WHE4012_G
	42	466.5	66.1	644	6	CD931399	CD931399 GR45.114G
	43	466.5	66.1	814	8	CV780906	CV780906 FGAS07531
	44	466.5	66.1	830	8	CV766226	CV766226 FGAS06061
	45	466.5	66.1	840	8	CV777091	CV777091 FGAS07149

ALIGNMENTS

RESULT 1
BI358791
LOCUS BI358791 443 bp mRNA linear EST 31-JUL-2001
DEFINITION 949040H08.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose Zea mays cDNA, mRNA sequence.
ACCESSION BI358791
VERSION BI358791.1 GI:15053246
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 443)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949040 row: H column: 08.
FEATURES Location/Qualifiers
source 1. .443
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"

/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative meristem"
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

ORIGIN

Alignment Scores:

Pred. No.:	9.13e-60	Length:	443
Score:	706.00	Matches:	143
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-759-548B-5 (1-143) x BI358791 (1-443)

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Qy          1 MetAlaLeuSerLeuSerLeuAlaArgProAlaProLeuAlaValSerAlaGlyAlaGly 20
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Db          1 ATGGCGCTGTCCCTCTCCCTCGCGCGCCCCGCGCCCCTCGCCGTTTCCGCCGGCGCAGGA 60

Qy         21 AlaArgLysLeuProAlaAlaSerLeuAlaPheProAlaLysSerPhePheGlyAlaPro 40
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Db         61 GCCAGGAAGCTACCCGCAGCCAGCCTCGCATTCCCGGCGAAATCCTTCTTCGGCGCGCCG 120

Qy         41 LeuAlaAlaThrAlaAlaSerValAlaSerProLeuProArgLysProAlaThrSerThr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGCCGCCACCGCGGCCTCCGTCGCGTCGCCGCTCCCGCGCAAGCCGGCCACCTCCACC 180

Qy         61 ThrSerLeuGluValValAlaAlaGlyLysLysGlyTyrLysMetLysThrHisLysAla 80
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Db        181 ACCTCGCTCGAGGTCGTCGCGGCGGGGAAGAAGGGCTACAAGATGAAGACGCACAAGGCG 240

Qy         81 SerAlaLysArgPheArgValThrGlyArgGlyLysIleValArgArgCysAlaGlyLys 100
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Db        241 TCGGCGAAGCGGTTCCGGGTGACGGGGAGGGGCAAGATCGTGCGGCGGTGCGCCGGGAAG 300

Qy        101 GlnHisLeuLeuAlaLysLysAsnThrLysArgLysLysArgLeuSerLysMetValGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCACTTGCTCGCCAAGAAGAACACCAAGCGCAAGAAGAGGCTCTCGAAGATGGTGCAA 360

Qy        121 ValAsnLysSerAspTyrAspAsnValThrGlyAlaLeuProTyrLeuLysValAsnArg 140
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Db        361 GTCAACAAGAGTGACTACGACAATGTTACGGGTGCACTGCCCTACCTCAAAGTGAATAGG 420

Qy        141 LysAlaAsn 143
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Db        421 AAAGCAAAC 429
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RESULT 2
BI478792/c

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LOCUS       BI478792                555 bp    mRNA    linear   EST 28-AUG-2001
DEFINITION  949070F06.x1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI478792
VERSION     BI478792.1  GI:15323570
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949070  row: F  column: 06.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex, including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN
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Alignment Scores:

Pred. No.:	1.22e-59	Length:	555
Score:	706.00	Matches:	143
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-759-548B-5 (1-143) x BI478792 (1-555)

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Qy          1 MetAlaLeuSerLeuSerLeuAlaArgProAlaProLeuAlaValSerAlaGlyAlaGly 20
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Db        527 ATGGCGCTGTCCCTCTCCCTCGCGCGCCCCGCGCCCCTCGCCGTTTCCGCCGGCGCAGGA 468

Qy         21 AlaArgLysLeuProAlaAlaSerLeuAlaPheProAlaLysSerPhePheGlyAlaPro 40
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Db        467 GCCAGGAAGCTACCCGCAGCCAGCCTCGCATTCCCGGCGAAATCCTTCTTCGGCGCGCCG 408

Qy         41 LeuAlaAlaThrAlaAlaSerValAlaSerProLeuProArgLysProAlaThrSerThr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 CTGGCCGCCACCGCGGCCTCCGTCGCGTCGCCGCTCCCGCGCAAGCCGGCCACCTCCACC 348

Qy         61 ThrSerLeuGluValValAlaAlaGlyLysLysGlyTyrLysMetLysThrHisLysAla 80
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Db        347 ACCTCGCTCGAGGTCGTCGCGGCGGGGAAGAAGGGCTACAAGATGAAGACGCACAAGGCG 288

Qy         81 SerAlaLysArgPheArgValThrGlyArgGlyLysIleValArgArgCysAlaGlyLys 100
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Db        287 TCGGCGAAGCGGTTCCGGGTGACGGGGAGGGGCAAGATCGTGCGGCGGTGCGCCGGGAAG 228
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Qy        101 GlnHisLeuLeuAlaLysLysAsnThrLysArgLysLysArgLeuSerLysMetValGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CAGCACTTACTCGCCAAGAAGAACACCAAACGCAAGAAGAGGCTCTCCAAGATGGTCCAA 383

Qy        121 ValAsnLysSerAspTyrAspAsnValThrGlyAlaLeuProTyrLeuLysValAsnArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GTCAACAAGAGTGACTACGACAATGTGACGGGTGCACTGCCCTACCTCAAAGTGAATAGG 443

Qy        141 LysAlaAsn 143
              |||||||||
Db        444 AAAGCAAAC 452

RESULT 11
BI233829
LOCUS       BI233829                430 bp    mRNA    linear   EST 11-JUL-2001
DEFINITION  949032H11.y2 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI233829
VERSION     BI233829.1  GI:14701411
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949032  row: H  column: 11.
FEATURES             Location/Qualifiers
     source          1. .430
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                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

Alignment Scores:
Pred. No.:              1.6e-56        Length:         430
Score:                  673.00         Matches:        135
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            95.3%          Indels:         0
DB:                     2              Gaps:           0

US-10-759-548B-5 (1-143) x BI233829 (1-430)

Qy          9 ArgProAlaProLeuAlaValSerAlaGlyAlaGlyAlaArgLysLeuProAlaAlaSer 28
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Db          2 CGCCCCGCGCCCCTCGCCGTTTCCGCCGGCGCAGGAGCCAGGAAGCTACCCGCAGCCAGC 61

Qy         29 LeuAlaProProAlaLysSerPhePheGlyAlaProLeuAlaAlaThrAlaAlaSerVal 48
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Db         62 CTCGCATTCCCGGCGAAATCCTTCTTCGGCGCGCCGCTGGCCGCCACCGCGGCCTCCGTC 121

Qy         49 AlaSerProLeuProArgLysProAlaThrSerThrThrSerLeuGluValValAlaAla 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GCGTCGCCGCTCCCGCGCAAGCCGGCCACCTCCACCACCTCGCTCGAGGTCGTCGCGGCG 181

Qy         69 GlyLysLysGlyTyrLysMetLysThrHisLysAlaSerAlaLysArgPheArgValThr 88
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Db        182 GGGAAGAAGGGCTACAAGATGAAGACGCACAAGGCGTCGGCGAAGCGGTTCCGGGTGACG 241

Qy         89 GlyArgGlyLysIleValArgArgCysAlaGlyLysGlnHisLeuLeuAlaLysLysAsn 108
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Db        242 GGGAGGGGCAAGATCGTGCGGCGGTGCGCCGGGAAGCAGCACTTGCTCGCCAAGAAGAAC 301

Qy        109 ThrLysArgLysLysArgLeuSerLysMetValGlnValAsnLysSerAspTyrAspAsn 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ACCAAGCGCAAGAAGAGGCTCTCGAAGATGGTGCAAGTCAACAAGAGTGACTACGACAAT 361

Qy        129 ValThrGlyAlaLeuProTyrLeuLysValAsnArgLysAlaAsn 143
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Db        362 GTTACGGGTGCACTGCCCTACCTCAAAGTGAATAGGAAAGCAAAC 406

RESULT 12
BG317125
LOCUS       BG317125                412 bp    mRNA    linear   EST 26-FEB-2001
DEFINITION  947025F08.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
            sequence.
ACCESSION   BG317125
VERSION     BG317125.1  GI:13126555
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 947025  row: F  column: 08.
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf and stem, including leaf base"
                     /dev_stage="2 week old seedling (3 leaves)"
                     /lab_host="XL1-Blue"
                     /clone_lib="947 - 2 week shoot from Barkan lab"
                     /note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
                     Site_1: EcoRI; Site_2: XhoI; Directionally cloned using
                     Stratagene's UniZap XR cDNA cloning kit with  the 5' end
                     at the EcoRI site. The library represents 8 x 10e5
                     independent recombinant phage. The plants were greenhouse
                     grown."
```